

SEQUENCE LISTING

<110> Boyce Thompson Institute for Plant Research

<120> BACTERIAL EFFECTOR PROTEINS WHICH INHIBIT PROGRAMMED
CELL DEATH

<130> 3213/102

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<150> 60/404,339

<151> 2002-08-16

<150> 60/425,842

<151> 2002-11-12

<160> 54

<170> PatentIn Ver. 2.1

<210> 1

<211> 1662

<212> DNA

<213> *Pseudomonas syringae*

<400> 1

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<210> 2

<211> 553

<212> PRT

<213> *Pseudomonas syringae*

<400> 2

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His Thr Asp Pro Glu Pro Val Ser Gly Gln Ala His Gly Ser Gly Ser
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Gly Ala Ser Ser Ser Asn Ser Pro Gln Val Gln Pro Arg Pro Ser Asn
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```

```

Thr Pro Pro Ser Asn Ala Pro Ala Pro Pro Pro Thr Gly Arg Glu Arg
      50             55             60

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Leu Ser Arg Ser Thr Ala Leu Ser Arg Gln Thr Arg Glu Trp Leu Glu
      65             70             75             80

```

```

Gln Gly Met Pro Thr Ala Glu Asp Ala Ser Val Arg Arg Arg Pro Gln
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```

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Val Thr Ala Asp Ala Ala Thr Pro Arg Ala Glu Ala Arg Arg Thr Pro
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Glu Ala Thr Ala Asp Ala Ser Ala Pro Arg Arg Gly Ala Val Ala His
      115            120            125

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Ala Asn Ser Ile Val Gln Gln Leu Val Ser Glu Gly Ala Asp Ile Ser
      130            135            140

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His Thr Arg Asn Met Leu Arg Asn Ala Met Asn Gly Asp Ala Val Ala
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Phe Ser Arg Val Glu Gln Asn Ile Phe Arg Gln His Phe Pro Asn Met
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Pro Met His Gly Ile Ser Arg Asp Ser Glu Leu Ala Ile Glu Leu Arg
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Gly Ala Leu Arg Arg Ala Val His Gln Gln Ala Ala Ser Ala Pro Val
 195 200 205

Arg Ser Pro Thr Pro Thr Pro Ala Ser Pro Ala Ala Ser Ser Ser Gly
 210 215 220

Ser Ser Gln Arg Ser Leu Phe Gly Arg Phe Ala Arg Leu Met Ala Pro
 225 230 235 240

Asn Gln Gly Arg Ser Ser Asn Thr Ala Ala Ser Gln Thr Pro Val Asp
 245 250 255

Arg Ser Pro Pro Arg Val Asn Gln Arg Pro Ile Arg Val Asp Arg Ala
 260 265 270

Ala Met Arg Asn Arg Gly Asn Asp Glu Ala Asp Ala Ala Leu Arg Gly
 275 280 285

Leu Val Gln Gln Gly Val Asn Leu Glu His Leu Arg Thr Ala Leu Glu
 290 295 300

Arg His Val Met Gln Arg Leu Pro Ile Pro Leu Asp Ile Gly Ser Ala
 305 310 315 320

Leu Gln Asn Val Gly Ile Asn Pro Ser Ile Asp Leu Gly Glu Ser Leu
 325 330 335

Val Gln His Pro Leu Leu Asn Leu Asn Val Ala Leu Asn Arg Met Leu
 340 345 350

Gly Leu Arg Pro Ser Ala Glu Arg Ala Pro Arg Pro Ala Val Pro Val
 355 360 365

Ala Pro Ala Thr Ala Ser Arg Arg Pro Asp Gly Thr Arg Ala Thr Arg
 370 375 380

Leu Arg Val Met Pro Glu Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr
 385 390 395 400

Gly Val Arg Leu Leu Asn Leu Asn Pro Gly Val Gly Val Arg Gln Ala
 405 410 415

Val Ala Ala Phe Val Thr Asp Arg Ala Glu Arg Pro Ala Val Val Ala
 420 425 430

Asn Ile Arg Ala Ala Leu Asp Pro Ile Ala Ser Gln Phe Ser Gln Leu
 435 440 445

Arg Thr Ile Ser Lys Ala Asp Ala Glu Ser Glu Glu Leu Gly Phe Lys
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Asp Ala Ala Asp His His Thr Asp Asp Val Thr His Cys Leu Phe Gly
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Gly Glu Leu Ser Leu Ser Asn Pro Asp Gln Gln Val Ile Gly Leu Ala
 485 490 495

Gly Asn Pro Thr Asp Thr Ser Gln Pro Tyr Ser Gln Glu Gly Asn Lys
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Asp Leu Ala Phe Met Asp Met Lys Lys Leu Ala Gln Phe Leu Ala Gly
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Ala Lys Tyr Ala Phe Arg Ile Val Pro
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<210> 3

<211> 1740

<212> DNA

<213> *Pseudomonas syringae*

<400> 3

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<210> 4

<211> 579

<212> PRT

<213> *Pseudomonas syringae*

<400> 4

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His Thr Asp Pro Glu Pro Ala Ser Gly Gly Ala His Gly Ser Ser Ser
      20             25             30

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```

Gly Ala Arg Ser Ser Asn Ser Pro Arg Leu Pro Ala Pro Pro Asp Ala
      35             40             45

```

```

Pro Ala Ser Gln Ala Arg Asp Arg Arg Glu Met Leu Leu Arg Ala Arg
      50             55             60

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Pro Leu Ser Arg Gln Thr Arg Glu Trp Val Ala Gln Gly Met Pro Pro
      65             70             75             80

```

```

Thr Ala Glu Ala Gly Val Pro Ile Arg Pro Gln Glu Ser Ala Glu Ala
      85             90             95

```

```

Ala Ala Pro Gln Ala Arg Ala Glu Glu Arg His Thr Pro Glu Ala Asp
      100            105            110

```

```

Ala Ala Ala Ser His Val Arg Thr Glu Gly Gly Arg Thr Pro Gln Ala
      115            120            125

```

```

Leu Ala Gly Thr Ser Pro Arg His Thr Gly Ala Val Pro His Ala Asn
      130            135            140

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Asn	Thr	Met	Ile	Asp	Asn	Ala	Met	Arg	Arg	His	Ala	Ile	Ala	Leu	Pro	165	170	175	
Ser	Arg	Thr	Val	Gln	Ser	Ile	Leu	Ile	Glu	His	Phe	Pro	His	Leu	Leu	180	185	190	
Ala	Gly	Glu	Leu	Ile	Ser	Gly	Ser	Glu	Leu	Ala	Thr	Ala	Phe	Arg	Ala	195	200	205	
Ala	Leu	Arg	Arg	Glu	Val	Arg	Gln	Gln	Glu	Ala	Ser	Ala	Pro	Pro	Arg	210	215	220	
Thr	Ala	Ala	Arg	Ser	Ser	Val	Arg	Thr	Pro	Glu	Arg	Ser	Thr	Val	Pro	225	230	235	240
Pro	Thr	Ser	Thr	Glu	Ser	Ser	Ser	Gly	Ser	Asn	Gln	Arg	Thr	Leu	Leu	245	250	255	
Gly	Arg	Phe	Ala	Gly	Leu	Met	Thr	Pro	Asn	Gln	Arg	Arg	Pro	Ser	Ser	260	265	270	
Ala	Ser	Asn	Ala	Ser	Ala	Ser	Gln	Arg	Pro	Val	Asp	Arg	Ser	Pro	Pro	275	280	285	
Arg	Val	Asn	Gln	Val	Pro	Thr	Gly	Ala	Asn	Arg	Val	Val	Met	Arg	Asn	290	295	300	
His	Gly	Asn	Asn	Glu	Ala	Asp	Ala	Ala	Leu	Gln	Gly	Leu	Ala	Gln	Gln	305	310	315	320
Gly	Val	Asp	Met	Glu	Asp	Leu	Arg	Ala	Ala	Leu	Glu	Arg	His	Ile	Leu	325	330	335	
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Gly	Ile	Ala	Pro	Ser	Ile	Asp	Thr	Gly	Glu	Ser	Leu	Met	Glu	Asn	Pro	355	360	365	
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Ala	Arg	Ala	Gln	Ala	Pro	Arg	Pro	Ala	Val	Pro	Val	Ala	Pro	Ala	Thr	385	390	395	400

Val Ser Arg Arg Pro Asp Ser Ala Arg Ala Thr Arg Leu Gln Val Ile
 405 410 415
 Pro Ala Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr Gly Val Arg Leu
 420 425 430
 Leu Ser Leu Asn Pro Gly Ala Gly Val Arg Glu Thr Val Ala Ala Phe
 435 440 445
 Val Asn Asn Arg Tyr Glu Arg Gln Ala Val Val Ala Asp Ile Arg Ala
 450 455 460
 Ala Leu Asn Leu Ser Lys Gln Phe Asn Lys Leu Arg Thr Val Ser Lys
 465 470 475 480
 Ala Asp Ala Ala Ser Asn Lys Pro Gly Phe Lys Asp Ala Ala Asp His
 485 490 495
 Pro Asp Asp Ala Thr Gln Cys Leu Phe Gly Glu Glu Leu Ser Leu Thr
 500 505 510
 Ser Ser Asp Gln Gln Val Ile Gly Leu Ala Gly Lys Ala Thr Asp Met
 515 520 525
 Ser Glu Ser Tyr Ser Arg Glu Ala Asn Lys Asp Leu Val Phe Met Asp
 530 535 540
 Met Lys Lys Leu Ala Gln Phe Leu Ala Gly Lys Pro Glu His Pro Met
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 Ile Val Pro

<210> 5

<211> 1740

<212> DNA

<213> Pseudomonas syringae

<220>

<221> unsure

<222> (1100)

<223> N at position 1100 can be A, C, T, or G

<400> 5

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<210> 6

<211> 579

<212> PRT

<213> *Pseudomonas syringae*

<220>

<221> UNSURE

<222> (367)

<223> Xaa at position 367 can be any amino acid

<400> 6

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His Thr Asp Pro Glu Pro Ala Ser Gly Gly Ala His Gly Ser Ser Ser
      20                   25                   30

```


Gly Ala Ser Ser Ser Asn Ser Pro Arg Leu Pro Ala Pro Pro Asp Ala
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 Pro Ala Ser Gln Ala Arg Asp Arg Arg Glu Met Leu Leu Arg Ala Arg
 50 55 60
 Pro Leu Ser Arg Gln Thr Arg Glu Trp Val Ala Gln Gly Met Pro Pro
 65 70 75 80
 Thr Ala Glu Ala Gly Val Pro Ile Arg Pro Gln Glu Ser Ala Glu Ala
 85 90 95
 Ala Ala Pro Gln Ala Arg Ala Glu Glu Arg His Thr Pro Glu Ala Asp
 100 105 110
 Ala Ala Ala Ser His Val Arg Thr Glu Gly Gly Arg Thr Pro Gln Ala
 115 120 125
 Leu Ala Gly Thr Ser Pro Arg His Thr Gly Ala Val Pro His Ala Asn
 130 135 140
 Arg Ile Val Gln Gln Leu Val Asp Ala Gly Ala Asp Leu Ala Gly Ile
 145 150 155 160
 Asn Thr Met Ile Asp Asn Ala Met Arg Arg His Ala Ile Ala Leu Pro
 165 170 175
 Ser Arg Thr Val Gln Ser Ile Leu Ile Glu His Phe Pro His Leu Leu
 180 185 190
 Ala Gly Glu Leu Ile Ser Gly Ser Glu Leu Ala Thr Ala Phe Arg Ala
 195 200 205
 Ala Leu Arg Arg Glu Val Arg Gln Gln Glu Ala Ser Ala Pro Pro Arg
 210 215 220
 Thr Thr Ala Arg Ser Ser Val Arg Thr Pro Glu Arg Ser Thr Val Pro
 225 230 235 240
 Pro Thr Ser Thr Glu Ser Ser Ser Gly Ser Asn Gln Arg Thr Leu Leu
 245 250 255
 Gly Arg Phe Ala Gly Leu Met Thr Pro Asn Gln Arg Arg Pro Ser Ser
 260 265 270
 Ala Ser Asn Ala Ser Ala Ser Gln Arg Pro Val Asp Arg Ser Pro Pro
 275 280 285

Arg Val Asn Gln Val Pro Thr Gly Ala Asn Arg Val Val Met Arg Asn
 290 295 300

His Gly Asn Asn Glu Ala Asp Ala Ala Leu Gln Gly Leu Ala Gln Gln
 305 310 315 320

Gly Val Asp Met Glu Asp Leu Arg Ala Ala Leu Glu Arg His Ile Leu
 325 330 335

His Arg Arg Pro Ile Pro Met Asp Ile Ala Tyr Ala Leu Gln Gly Val
 340 345 350

Gly Ile Ala Pro Ser Ile Asp Thr Gly Glu Ser Leu Met Glu Xaa Pro
 355 360 365

Leu Met Asn Leu Ser Val Ala Leu His Arg Ala Leu Gly Pro Arg Pro
 370 375 380

Ala Arg Ala Gln Ala Pro Arg Pro Ala Val Pro Val Ala Pro Ala Thr
 385 390 395 400

Val Ser Arg Arg Pro Asp Ser Ala Arg Ala Thr Arg Leu Gln Val Ile
 405 410 415

Pro Ala Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr Gly Val Arg Leu
 420 425 430

Leu Ser Leu Asn Pro Gly Ala Trp Val Arg Glu Thr Val Ala Ala Phe
 435 440 445

Val Asn Asn Arg Tyr Glu Arg Gln Ala Val Val Ala Asp Ile Arg Ala
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Ala Leu Asn Leu Ser Lys Gln Phe Asn Lys Leu Arg Thr Val Ser Lys
 465 470 475 480

Ala Asp Ala Ala Ser Asn Lys Pro Gly Phe Lys Asp Leu Ala Asp His
 485 490 495

Pro Asp Asp Ala Thr Gln Cys Leu Phe Gly Glu Glu Leu Ser Leu Thr
 500 505 510

Ser Ser Val Gln Gln Val Ile Gly Leu Ala Gly Lys Ala Thr Asp Met
 515 520 525

Ser Glu Ser Tyr Ser Arg Glu Ala Asn Lys Asp Leu Val Phe Met Asp
 530 535 540

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Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile Ala Lys Tyr Ala Phe Arg
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Ile Val Pro

<210> 7

<211> 1740

<212> DNA

<213> *Pseudomonas syringae*

<400> 7

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<210> 8

<211> 579

<212> PRT

<213> *Pseudomonas syringae*

<400> 8

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Met Ala Gly Ile Asn Gly Ala Gly Pro Ser Gly Ala Tyr Phe Val Gly
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His Thr Asp Pro Glu Pro Ala Ser Gly Gly Ala His Gly Ser Ser Ser
      20             25             30

Gly Ala Ser Ser Ser Asn Ser Pro Arg Leu Pro Ala Pro Pro Asp Ala
      35             40             45

Pro Ala Ser Gln Ala Arg Asp Arg Arg Glu Met Leu Leu Arg Ala Arg
      50             55             60

Pro Leu Ser Arg Gln Thr Arg Glu Trp Val Ala Gln Gly Met Pro Pro
      65             70             75             80

Thr Ala Glu Ala Gly Val Pro Ile Arg Pro Gln Glu Ser Ala Glu Ala
      85             90             95

Ala Ala Pro Gln Ala Arg Ala Glu Glu Arg His Thr Pro Glu Ala Asp
      100            105            110

Ala Ala Ala Ser His Val Arg Thr Glu Gly Gly Arg Thr Pro Gln Ala
      115            120            125

Leu Ala Gly Thr Ser Pro Arg His Thr Gly Ala Val Pro His Ala Asn
      130            135            140

Arg Ile Val Gln Gln Leu Val Asp Ala Gly Ala Asp Leu Ala Gly Ile
      145            150            155            160

Asn Thr Met Ile Asp Asn Ala Met Arg Arg His Ala Ile Ala Leu Pro
      165            170            175

Ser Arg Thr Val Gln Ser Ile Leu Ile Glu His Phe Pro His Leu Leu
      180            185            190

Ala Gly Glu Leu Ile Ser Gly Ser Glu Leu Ala Thr Ala Phe Arg Ala
      195            200            205

Ala Leu Arg Arg Glu Val Arg Gln Gln Glu Ala Ser Ala Pro Pro Arg
      210            215            220

Thr Ala Ala Arg Ser Ser Val Arg Thr Pro Glu Arg Ser Thr Val Pro

```

225		230		235		240
Pro Thr Ser Thr Glu Ser Ser Ser Gly Ser Asn Gln Arg Thr Leu Leu						
	245		250		255	
Gly Arg Phe Ala Gly Leu Met Thr Pro Asn Gln Arg Arg Pro Ser Ser						
	260		265		270	
Ala Ser Asn Ala Ser Ala Ser Gln Arg Pro Val Asp Arg Ser Pro Pro						
	275		280		285	
Arg Val Asn Gln Val Pro Thr Gly Ala Asn Arg Val Val Met Arg Asn						
	290		295		300	
His Gly Asn Asn Glu Ala Asp Ala Ala Leu Gln Gly Leu Ala Gln Gln						
305		310		315		320
Gly Val Asp Met Glu Asp Leu Arg Ala Ala Leu Glu Arg His Ile Leu						
	325		330		335	
His Arg Arg Pro Ile Pro Met Asp Ile Ala Tyr Ala Leu Gln Gly Val						
	340		345		350	
Gly Ile Ala Pro Ser Ile Asp Thr Gly Glu Ser Leu Met Glu Asn Pro						
	355		360		365	
Leu Met Asn Leu Ser Val Ala Leu His Arg Ala Leu Gly Pro Arg Pro						
	370		375		380	
Ala Arg Ala Gln Ala Pro Arg Pro Ala Val Pro Val Ala Pro Ala Thr						
385		390		395		400
Val Ser Arg Arg Pro Asp Ser Ala Arg Ala Thr Arg Leu Gln Val Ile						
	405		410		415	
Pro Ala Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr Gly Val Arg Leu						
	420		425		430	
Leu Ser Leu Asn Pro Gly Ala Gly Val Arg Glu Thr Val Ala Ala Phe						
	435		440		445	
Val Asn Asn Arg Tyr Glu Arg Gln Ala Val Val Ala Asp Ile Arg Ala						
	450		455		460	
Ala Leu Asn Leu Ser Lys Gln Phe Asn Lys Leu Arg Thr Val Ser Lys						
465		470		475		480
Ala Asp Ala Ala Ser Asn Lys Pro Gly Phe Lys Asp Leu Ala Asp His						

<400> 11
Leu Ser Arg Gln Thr Arg Glu Trp

1

5

<210> 12

<211> 6

<212> PRT

<213> Pseudomonas syringae

<400> 12

Ile Val Gln Gln Leu Val

1

5

<210> 13

<211> 5

<212> PRT

<213> Pseudomonas syringae

<400> 13

Ser Ser Ser Gly Ser

1

5

<210> 14

<211> 11

<212> PRT

<213> Pseudomonas syringae

<400> 14

Pro Val Asp Arg Ser Pro Pro Arg Val Asn Gln

1

5

10

<210> 15

<211> 12

<212> PRT

<213> Pseudomonas syringae

<400> 15

Ala Pro Arg Pro Ala Val Pro Val Ala Pro Ala Thr

1

5

10

<210> 16

<211> 5

<212> PRT

<213> Pseudomonas syringae

<400> 16

Ser Arg Arg Pro Asp

1 5

<210> 17

<211> 5

<212> PRT

<213> Pseudomonas syringae

<400> 17

Arg Ala Thr Arg Leu

1 5

<210> 18

<211> 15

<212> PRT

<213> Pseudomonas syringae

<400> 18

Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr Gly Val Arg Leu Leu

1 5 10 15

<210> 19

<211> 5

<212> PRT

<213> Pseudomonas syringae

<400> 19

Val Ala Ala Phe Val

1 5

<210> 20

<211> 5

<212> PRT

<213> Pseudomonas syringae

<400> 20

Ile Arg Ala Ala Leu

1 5

<210> 21

<211> 5

<212> PRT

<213> Pseudomonas syringae

<400> 21

Ser Lys Ala Asp Ala

1 5

<210> 22

<211> 8

<212> PRT

<213> Pseudomonas syringae

<400> 22

Gln Gln Val Ile Gly Leu Ala Gly

1 5

<210> 23

<211> 38

<212> PRT

<213> Pseudomonas syringae

<400> 23

Phe Met Asp Met Lys Lys Leu Ala Gln Phe Leu Ala Gly Lys Pro Glu

1 5 10 15

His Pro Met Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile Ala Lys Tyr

20 25 30

Ala Phe Arg Ile Val Pro

35

<210> 24

<211> 553

<212> PRT

<213> Pseudomonas syringae

<220>

<221> UNSURE

<222> (1)..(6)

<223> Xaa at positions 1-6 can be any amino acid

<220>

<221> UNSURE

<222> (23)..(31)

<223> Xaa at positions 23-31 can be any amino acid

<220>
<221> UNSURE
<222> (41)..(70)
<223> Xaa at positions 41-70 can be any amino acid

<220>
<221> UNSURE
<222> (79)..(131)
<223> Xaa at positions 79-131 can be any amino acid

<220>
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<222> (138)..(220)
<223> Xaa at positions 138-220 can be any amino acid

<220>
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<222> (226)..(253)
<223> Xaa at positions 226-253 can be any amino acid

<220>
<221> UNSURE
<222> (265)..(360)
<223> Xaa at positions 265-360 can be any amino acid

<220>
<221> UNSURE
<222> (373)
<223> Xaa at position 373 can be any amino acid

<220>
<221> UNSURE
<222> (379)..(380)
<223> Xaa at positions 379-380 can be any amino acid

<220>
<221> UNSURE
<222> (386)..(390)
<223> Xaa at positions 386-390 can be any amino acid

<220>
<221> UNSURE
<222> (406)..(433)
<223> Xaa at positions 406-433 can be any amino acid

<220>
<221> UNSURE
<222> (439)..(451)

<223> Xaa at positions 439-451 can be any amino acid

<220>

<221> UNSURE

<222> (457)..(489)

<223> Xaa at positions 457-489 can be any amino acid

<220>

<221> UNSURE

<222> (498)..(515)

<223> Xaa at positions 498-515 can be any amino acid

<400> 24

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Gly	Pro	Ser	Gly	Ala	Tyr	Phe	Val	Gly
1					5					10					15

His	Thr	Asp	Pro	Glu	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser
			20					25						30	

Gly	Ala	Ser	Ser	Ser	Asn	Ser	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40						45		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		50					55				60				

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Ser	Arg	Gln	Thr	Arg	Glu	Trp	Xaa	Xaa
65						70				75					80

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
					85				90					95	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105					110		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		115					120					125			

Xaa	Xaa	Xaa	Ile	Val	Gln	Gln	Leu	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		130				135					140				

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
145					150				155					160	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			165					170					175		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		180						185					190		

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ser Ser Gly
 210 215 220

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 225 230 235 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Val Asp
 245 250 255

Arg Ser Pro Pro Arg Val Asn Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 260 265 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 275 280 285

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 290 295 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 305 310 315 320

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 325 330 335

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 340 345 350

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Pro Arg Pro Ala Val Pro Val
 355 360 365

Ala Pro Ala Thr Xaa Ser Arg Arg Pro Asp Xaa Xaa Arg Ala Thr Arg
 370 375 380

Leu Xaa Xaa Xaa Xaa Xaa Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr
 385 390 395 400

Gly Val Arg Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 405 410 415

Val Ala Ala Phe Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 420 425 430

Xaa Ile Arg Ala Ala Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 435 440 445

Xaa Xaa Xaa Ser Lys Ala Asp Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 450 455 460

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 465 470 475 480

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln Val Ile Gly Leu Ala
 485 490 495

Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 500 505 510

Xaa Xaa Xaa Phe Met Asp Met Lys Lys Leu Ala Gln Phe Leu Ala Gly
 515 520 525

Lys Pro Glu His Pro Met Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile
 530 535 540

Ala Lys Tyr Ala Phe Arg Ile Val Pro
 545 550

<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 25

gtaatgcagc gcctccctat c

21

<210> 26

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 26

tcaggggact attctaaaag c

21

<210> 27

<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 27

atggcgggta tcaatagagc g

21

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 28

tcacacccgc aatcgtgttg cac

23

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 29

tcatacatgt ctttcaaggg ccg

23

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 30

gtatcaatag agcgggacca tc

22

<210> 31

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 31

cactgaccac ttgctgaacg

20

<210> 32

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 32

tgtcgcgcca aaccagggcg tg

22

<210> 33

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 33

ccatcaccag ggcaaacc

18

<210> 34

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 34

gtatcgttca gcaattggtc agtg

24

<210> 35

<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 35
acgcgtatgg gtctttggtt g

21

<210> 36
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 36
acgattgcgg gtgatgc

17

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 37
cctcttggct gtaaggctgc

20

<210> 38
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 38
atggcgggta tcaatagagc gg

22

<210> 39

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 39

gaattcgata tcaagcttat cgataccgtc gacctcgag

39

<210> 40

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 40

gaattcgaat tgggatatca agcttatcga taccgtcgac ctcgag

46

<210> 41

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 41

gaattcgaat tgatatcaag cttatcgata ccgtcgacct cgag

44

<210> 42

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 42

cggaggcgaa cagccgagca g

21

<210> 43

<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 43
gcaattcgaa gtggcagtga

20

<210> 44
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44
ttatgcttta ttggtatddd tagagg

26

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 45
atggcgggta tcaatagagc

20

<210> 46
<211> 26
<212> DNA
<213> Pseudomonas syringae

<220>

<221> unsure

<222> (7)..(22)

<223> N at positions 7-22 can be A, C, T, or G

<400> 46
ggaactnnnn nnnnnnnnnn nccac

26

<210> 47
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 47
Met Ala Gly Ile Asn Arg Ala Gly
1 5

<210> 48
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence

<220>
<221> UNSURE
<222> (2)
<223> Xaa at position 2 can be any amino acid except E

<220>
<221> UNSURE
<222> (3)
<223> Xaa at position 3 can be any amino acid except D

<220>
<221> UNSURE
<222> (4)
<223> Xaa at position 4 can be any amino acid except R

<220>
<221> UNSURE
<222> (5)
<223> Xaa at position 5 can be any amino acid except K

<220>
<221> UNSURE
<222> (6)
<223> Xaa at position 6 can be any amino acid except H

<220>

<221> UNSURE

<222> (7)

<223> Xaa at position 7 can be any amino acid except P

<220>

<221> UNSURE

<222> (8)

<223> Xaa at position 8 can be any amino acid except F

<220>

<221> UNSURE

<222> (9)

<223> Xaa at position 9 can be any amino acid except Y

<220>

<221> UNSURE

<222> (10)

<223> Xaa at position 10 can be any amino acid except W

<220>

<221> UNSURE

<222> (11)..(12)

<223> Xaa at positions 11-12 can be any amino acid

<220>

<221> UNSURE

<222> (19)

<223> Xaa at position 19 can be any amino acid except P

<400> 48

Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Thr Ala Gly

1

5

10

15

Cys Asn Xaa

<210> 49

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

<220>

<221> UNSURE
<222> (2)..(3)
<223> Xaa at positions 2-3 can be any amino acid

<220>
<221> UNSURE
<222> (5)..(6)
<223> Xaa at positions 5-6 can be any amino acid

<220>
<221> UNSURE
<222> (8)..(9)
<223> Xaa at positions 8-9 can be any amino acid

<220>
<221> UNSURE
<222> (11)
<223> Xaa at position 11 can be any amino acid

<220>
<221> UNSURE
<222> (13)..(15)
<223> Xaa at positions 13-15 can be any amino acid

<400> 49
Arg Xaa Xaa Leu Xaa Xaa Ser Xaa Xaa Leu Xaa Arg Xaa Xaa Xaa Glu
1 5 10 15

<210> 50
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence

<220>
<221> UNSURE
<222> (2)
<223> Xaa at position 2 can be any amino acid

<220>
<221> UNSURE
<222> (4)
<223> Xaa at position 4 can be any amino acid

<400> 50

Ser Xaa Arg Xaa Arg
 1 5

<210> 51

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
 sequence

<220>

<221> UNSURE

<222> (4)..(8)

<223> Xaa at positions 4-8 can be any amino acid

<400> 51

Asn Pro Ser Xaa Xaa Xaa Xaa Xaa Ser
 1 5

<210> 52

<211> 539

<212> PRT

<213> Pseudomonas syringae

<400> 52

Met Pro Gly Ile Asn Gly Ala Gly Pro Ser Asn Phe Phe Trp Gln Trp
 1 5 10 15

Arg Thr Asp Gly Glu Pro Val Thr Glu Arg Glu His Asp Ser Ser Arg
 20 25 30

Ser Ala Ser Ser Ala Asn Ser Pro Glu Leu Pro Pro Pro Ala Ser Pro
 35 40 45

Ala Glu Ser Gly Arg Gln Arg Leu Leu Arg Ser Ser Ala Leu Ser Arg
 50 55 60

Gln Thr Arg Glu Trp Leu Glu Ala Thr Pro Ala Arg Val Gln Gly Ala
 65 70 75 80

Thr Pro Pro Ala Glu Ala Arg Gln Ser Pro Glu Ala Gln Gln Ala Glu
 85 90 95

Arg Ile Val Gln Glu Leu Val Arg Gly Gly Ala Asp Leu Asn Asn Val	100	105	110
Arg Thr Met Leu Arg Asn Val Met Asp Asn Asn Ala Val Ala Phe Ser	115	120	125
Arg Val Glu Arg Asp Ile Leu Leu Gln His Phe Pro Asn Met Pro Met	130	135	140
Thr Gly Ile Ser Ser Asp Ser Val Leu Ala Asn Glu Leu Arg Gln Arg	145	150	155
Leu Arg Gln Thr Val Arg Gln Gln Arg Ile Gln Ser Ser Thr Pro Ala	165	170	175
Arg Leu Ala Asp Ser Ser Ser Gly Ser Ser Gln Arg Ser Leu Ile Gly	180	185	190
Arg Ser Thr Met Leu Met Thr Pro Gly Arg Ser Ser Ser Ser Ser Ala	195	200	205
Ala Ala Ser Arg Thr Ser Val Asp Arg His Pro Gln Gly Leu Asp Leu	210	215	220
Glu Ser Ala Arg Leu Ala Ser Ala Ala Arg His Asn His Ser Ala Asn	225	230	235
Gln Thr Asn Glu Ala Leu Arg Arg Leu Thr Gln Glu Gly Val Asp Met	245	250	255
Glu Arg Leu Arg Thr Ser Leu Gly Arg Tyr Ile Met Ser Leu Glu Pro	260	265	270
Leu Pro Pro Asp Leu Arg Arg Ala Leu Glu Ser Val Gly Ile Asn Pro	275	280	285
Phe Ile Pro Glu Glu Leu Ser Leu Val Asp His Pro Val Leu Asn Phe	290	295	300
Ser Ala Ala Leu Asn Arg Met Leu Ala Ser Arg Gln Thr Thr Thr Asn	305	310	315
Ser Pro Glu Leu Pro Pro Leu Ala Ser Ser Ala Glu Ser Gly Arg Arg	325	330	335
Arg Leu Leu Arg Ser Pro Pro Leu Leu Ser Gly Gln Arg Glu Trp Ile	340	345	350

Glu Gln Ser Met Arg Gln Glu Ala Glu Pro Gln Ser Ser Arg Leu Asn
 355 360 365

Arg Ala Val Arg Leu Ala Val Met Pro Pro Gln Asn Glu Asn Glu Asp
 370 375 380

Asn Val Ala Tyr Ala Ile Arg Leu Arg Arg Leu Asn Pro Gly Ala Asp
 385 390 395 400

Val Ser Arg Val Val Ala Ser Phe Ile Thr Asp Pro Ala Ala Arg Gln
 405 410 415

Gln Val Val Asn Asp Ile Arg Ala Ala Leu Asp Ile Ala Pro Gln Phe
 420 425 430

Ser Gln Leu Arg Thr Ile Ser Lys Ala Asp Ala Glu Ser Glu Glu Leu
 435 440 445

Gly Phe Arg Asp Ala Ala Asp His Pro Asp Asn Ala Thr Ser Cys Leu
 450 455 460

Phe Gly Glu Glu Leu Ser Leu Ser Asn Pro Asp Gln Gln Val Ile Gly
 465 470 475 480

Leu Ala Val Asn Pro Thr Asp Lys Pro Gln Pro Tyr Ser Gln Glu Val
 485 490 495

Asn Lys Ala Leu Thr Phe Met Asp Met Lys Lys Leu Ala Gln Tyr Leu
 500 505 510

Ala Asp Lys Pro Glu His Pro Leu Asn Arg Gln Arg Leu Asp Ala Lys
 515 520 525

Asn Ile Ala Lys Tyr Ala Phe Lys Ile Val Pro
 530 535

<210> 53

<211> 158

<212> PRT

<213> *Pseudomonas syringae*

<400> 53

Met Gly Asn Ile Cys Val Gly Gly Ser Arg Met Ala His Gln Val Asn
 1 5 10 15

Ser Pro Asp Arg Val Ser Asn Asn Ser Gly Asp Glu Asp Asn Val Thr
 20 25 30

Ser Ser Gln Leu Leu Ser Val Arg His Gln Leu Ala Glu Ser Ala Gly
 35 40 45
 Leu Pro Arg Asp Gln His Glu Phe Val Ser Ser Gln Ala Pro Gln Ser
 50 55 60
 Leu Arg Asn Arg Tyr Asn Asn Leu Tyr Ser His Thr Gln Arg Thr Leu
 65 70 75 80
 Asp Met Ala Asp Met Gln His Arg Tyr Met Thr Gly Ala Ser Gly Ile
 85 90 95
 Asn Pro Gly Met Leu Pro His Glu Asn Val Asp Asp Met Arg Ser Ala
 100 105 110
 Ile Thr Asp Trp Ser Asp Met Arg Glu Ala Leu Gln His Ala Met Gly
 115 120 125
 Ile His Ala Asp Ile Pro Pro Ser Pro Glu Arg Phe Val Ala Thr Met
 130 135 140
 Asn Pro Ser Gly Ser Ile Arg Met Ser Thr Leu Ser Pro Ser
 145 150 155

<210> 54

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

<220>

<221> UNSURE

<222> (2)

<223> Xaa at position 2 can be any amino acid

<220>

<221> UNSURE

<222> (4)..(5)

<223> Xaa at positions 4-5 can be any amino acid

<220>

<221> UNSURE

<222> (7)..(8)

<223> Xaa at positions 7-8 can be any amino acid

<220>

<221> UNSURE

<222> (10)..(11)

<223> Xaa at positions 10-11 can be any amino acid

<220>

<221> UNSURE

<222> (13)

<223> Xaa at position 13 can be any amino acid

<220>

<221> UNSURE

<222> (15)..(17)

<223> Xaa at positions 15-17 can be any amino acid

<400> 54

Ser	Xaa	Arg	Xaa	Xaa	Leu	Xaa	Xaa	Ser	Xaa	Xaa	Leu	Xaa	Arg	Xaa	Xaa
1					5				10					15	

Xaa Glu